

SEQUENCE LISTING

<110> CuraGen Corporation et al.

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<120> COMPOSITIONS AND METHODS OF USE FOR A FIBROBLAST GROWTH FACTOR

<130> 15966-557 SNP NATL (Cura-57 SNP NATL)

<140> 10.578,234

<141> 2004-11-03

<150> 10/702,126

<151> 2003-11-04

<160> 24

<170> CuraSeqList version 0.1

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Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu	
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Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
65 70 75 80	

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Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
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atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt	336
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly	
100 105 110	

gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat	384
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
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gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa	432
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
130 135 140	
gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac	480
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp	
145 150 155 160	
act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga	528
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg	
165 170 175	
gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct	576
Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro	
180 185 190	
aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag aac cta ctg	624
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Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
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Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
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Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly	
100 105 110	
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
115 120 125	
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
130 135 140	

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
 145 150 155 160
 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
 165 170 175
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 Met Tyr Thr
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 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
 35 40 45
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 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
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 cgc cgc ccg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg 240
 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
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 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
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 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
 100 105 110
 gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat 384
 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
 115 120 125
 gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa 432
 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
 130 135 140

gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac 480
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 145 150 155 160

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 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
 165 170 175

gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct 576
 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
 180 185 190

aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac cta ctg 624
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atg tac act 633
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 35 40 45

Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
 50 55 60

Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
 65 70 75 80

Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
 85 90 95

Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
 100 105 110

Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
 115 120 125

Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
 130 135 140

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
 145 150 155 160

Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
 165 170 175

Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
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Met Tyr Thr
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 tac tgc cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt 96
 Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val
 20 25 30
 cag ggt acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc 144
 Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile
 35 40 45
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 Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu
 50 55 60
 tac ctg ggt atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg 240
 Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu
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 acc tct gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac 288
 Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn
 85 90 95
 acc tac tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac 336
 Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr
 100 105 110
 ttc gtt gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct 384
 Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser
 115 120 125
 aaa cgt cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg 432
 Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro
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Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile
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 50              55              60

Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu
 65              70              75              80

Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn
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Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr
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Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser
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Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro
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ttg ggc cag ccg ggg gca gcg cag ctg gcg cac ctg cac ggc atc ctg      96
Leu Gly Gln Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
          20              25              30

cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg      144
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
          35              40              45

ccc gac ggc agc gcg cag ggc acc cgg cag gac cac agc ctc ttc ggt      192
Pro Asp Gly Ser Ala Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
          50              55              60

atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt      240
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
 65              70              75              80

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gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa	336
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
100 105 110	
gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac	384
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp	
115 120 125	
act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga	432
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg	
130 135 140	
gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct	480
Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro	
145 150 155 160	
aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag aac cta ctg	528
Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu	
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35 40 45															
Pro Asp Gly Ser Ala Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly															
50 55 60															
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly															
65 70 75 80															
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr															
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Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu															
100 105 110															
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp															
115 120 125															
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg															
130 135 140															

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 35 40 45
 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
 50 55 60

Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
 65 70 75 80
 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
 85 90 95
 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
 100 105 110
 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
 115 120 125
 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
 130 135 140
 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
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 165 170 175
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 Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro
 20 25 30
 cca ctg ctg ggt gaa cgt cgc tcc gca gct gaa cgc tcc gct cgt ggt 144
 Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly
 35 40 45
 ggc ccg ggt gct gct cag ctg gct cac ctg cat ggt atc ctg cgt cgc 192
 Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg
 50 55 60
 cgt cag ctg tac tgc cgt act ggt ttc cac ctg cag atc ctg ccg gat 240
 Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp
 65 70 75 80
 ggt tct gtt cag ggt acc cgt cag gac cac tct ctg ttc ggt atc ctg 288
 Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu
 85 90 95
 gaa ttc atc tct gtt gct gtt ggt ctg gtt tct atc cgt ggt gtt gac 336
 Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp

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115	120	125	
gaa aaa ctg acc tct gaa tgc atc ttc cgt gaa cag ttt gaa gag aac			432
Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn			
130	135	140	
tgg tac aac acc tac tct tcc aac atc tac aaa cat ggt gac acc ggc			480
Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly			
145	150	155	160
cgt cgc tac ttc gtt gct ctg aac aaa gac ggt acc ccg cgt gat ggt			528
Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly			
165	170	175	
gct cgt tct aaa cgt cac cag aaa ttc acc cac ttc ctg ccg cgc cca			576
Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro			
180	185	190	
gtt gac ccg gag cgt gtt cca gaa ctg tat aaa aac ctg ctg atg tac			624
Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr			
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acc taa			630
Thr			

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 35 40 45
 Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg
 50 55 60
 Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp
 65 70 75 80
 Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu
 85 90 95
 Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp
 100 105 110
 Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser
 115 120 125
 Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn

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Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly		
	165	170 175
Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro		
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Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr		
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Thr

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ttc ctg ctg ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt	96
Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg	
20 25 30	
cgc tcc gca gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct cag	144
Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln	
35 40 45	
ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt	192
Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg	
50 55 60	
act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc	240
Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr	
65 70 75 80	
cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct	288
Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala	
85 90 95	
gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt	336
Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly	
100 105 110	
atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa	384
Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu	
115 120 125	
tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct	432
Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser	

130	135	140	
tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt gct			480
Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala			
145	150	155	160
ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac			528
Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His			
	165	170	175
cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt			576
Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val			
	180	185	190
cca gaa ctg tat aaa aac ctg ctg atg tac acc taa			612
Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr			
	195	200	
<210> 15			
<211> 203			
<212> PRT			
<213> Homo sapiens			
<400> 15			
Gly Phe Leu Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His			
1	5	10	15
Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg			
	20	25	30
Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln			
	35	40	45
Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg			
	50	55	60
Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr			
	65	70	75
Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala			
	85	90	95
Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly			
	100	105	110
Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu			
	115	120	125
Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser			
	130	135	140
Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala			
	145	150	155
Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His			
	165	170	175
Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val			
	180	185	190
Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr			

195

200

<210> 16
 <211> 603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(600)

<400> 16

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ggc ggt ctg gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg      48
Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu
  1              5              10              15

ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca      96
Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala
              20              25              30

gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac     144
Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His
              35              40              45

ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc     192
Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe
              50              55              60

cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac     240
His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp
              65              70              75              80

cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg     288
His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu
              85              90              95

gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac     336
Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp
              100             105             110

aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc     384
Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe
              115             120             125

cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc     432
Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile
              130             135             140

tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa     480
Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys
              145             150             155             160

gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc     528
Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe
              165             170             175

acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg     576
Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu
              180             185             190

tat aaa aac ctg ctg atg tac acc taa                                603

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Tyr Lys Asn Leu Leu Met Tyr Thr
 195 200

<210> 17
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 17
 Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu
 1 5 10 15
 Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala
 20 25 30
 Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His
 35 40 45
 Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe
 50 55 60
 His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp
 65 70 75 80
 His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu
 85 90 95
 Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp
 100 105 110
 Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe
 115 120 125
 Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile
 130 135 140
 Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys
 145 150 155 160
 Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe
 165 170 175
 Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu
 180 185 190
 Tyr Lys Asn Leu Leu Met Tyr Thr
 195 200

<210> 18
 <211> 594
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(591)

<400> 18
 gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg ccg ccg gct 48
 Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala
 1 5 10 15

ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca gct gaa cgc	96
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg	
20 25 30	
tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac ctg cat ggt	144
Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly	
35 40 45	
atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc cac ctg cag	192
Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln	
50 55 60	
atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac cac tct ctg	240
Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu	
65 70 75 80	
ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg gtt tct atc	288
Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile	
85 90 95	
cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac aaa ggc gaa	336
Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu	
100 105 110	
ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc cgt gaa cag	384
Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln	
115 120 125	
ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc tac aaa cat	432
Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His	
130 135 140	
ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa gac ggt acc	480
Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr	
145 150 155 160	
ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc acc cac ttc	528
Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe	
165 170 175	
ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg tat aaa aac	576
Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn	
180 185 190	
ctg ctg atg tac acc taa	594
Leu Leu Met Tyr Thr	
195	
<210> 19	
<211> 197	
<212> PRT	
<213> Homo sapiens	
<400> 19	
Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala	
1 5 10 15	
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg	
20 25 30	

Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly
 35 40 45
 Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln
 50 55 60
 Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu
 65 70 75 80
 Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile
 85 90 95
 Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu
 100 105 110
 Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln
 115 120 125
 Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His
 130 135 140
 Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr
 145 150 155 160
 Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe
 165 170 175
 Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn
 180 185 190
 Leu Leu Met Tyr Thr
 195

<210> 20
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(564)

<400> 20
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 His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu
 1 5 10 15
 cgt cgc tcc gca gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct 96
 Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala
 20 25 30
 cag ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc 144
 Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys
 35 40 45
 cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt 192
 Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly
 50 55 60
 acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt 240
 Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val

65	70	75	80	
gct gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg	288			
Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu				
85 90 95				
ggt atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct	336			
Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser				
100 105 110				
gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac	384			
Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr				
115 120 125				
tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt	432			
Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val				
130 135 140				
gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt	480			
Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg				
145 150 155 160				
cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt	528			
His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg				
165 170 175				
gtt cca gaa ctg tat aaa aac ctg ctg atg tac acc taa	567			
Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr				
180 185				

<210> 21

<211> 188

<212> PRT

<213> Homo sapiens

<400> 21

His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu	
1 5 10 15	
Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala	
20 25 30	
Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys	
35 40 45	
Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly	
50 55 60	
Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val	
65 70 75 80	
Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu	
85 90 95	
Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser	
100 105 110	
Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr	
115 120 125	
Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val	

130 135 140

Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg
 145 150 155 160

His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg
 165 170 175

Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr
 180 185

<210> 22
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 22
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 ggcagcgtgc agggcaccgc gcaggaccac agcctcttcg gtatcttgga attcatcagt 120
 gtggcagtg gactggtcag tattagaggt gtggacagtg gtctctatct tggaatgaat 180
 gacaaaggag aactctatgg atcagagaaa cttacttccg aatgcatctt tagggagcag 240
 tttgaagaga actggtataa cacctattca tctaacatat ataaacatgg agacactggc 300
 cgcaggtatt ttgtggcact taacaaagac ggaactccaa gagatggcgc caggtccaag 360
 aggcacaga aatttacaca tttcttacct agaccagtgg atccagaaaa agttccagaa 420
 ttgtacaagg acctactgat gtacact 447

<210> 23
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 23
 Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln
 1 5 10 15

Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu
 20 25 30

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile
 35 40 45

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu
 50 55 60

Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln
 65 70 75 80

Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His
 85 90 95

Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr
 100 105 110

Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe
 115 120 125

Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn
 130 135 140

Leu Leu Met Tyr Thr
 145

<210> 24
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 24
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 ggggcagcgc agctggcgca cctgcacggc atcctgcgcc gccggcagct ctattgccgc 120
 accggcttcc acctgcagat cctgcccgac ggcagcgtgc agggcacccg gcaggaccac 180
 agcctcttcg gtatcttgga attcatcagt gtggcagtgg gactggtcag tattagaggt 240
 gtggacagtg gtctctatct tggaatgaat gacaaaggag aactctatgg atcagagaaa 300
 cttacttccg aatgcatctt tagggagcag tttgaagaga actggtataa cacctattca 360
 tctaacatat ataaacatgg agacactggc cgcaggtatt ttgtggcact taacaaagac 420
 ggaactccaa gagatggcgc caggtccaag aggcatacaga aatttacaca tttcttacct 480
 agaccagtgg atccagaaag agttccagaa ttgtacaaga acctactgat gtacact 537